

Riggs Supplemental Table ST4. Note that gene ontology (GO) categories overlapped (OVRLP), but the specific genes in those categories in IPS and OF were distinct.

IPS GO	# IPS genes	IPS Genes in category	IPS GOP	OF GO	# OF genes	OF Genes in category	OF GOP	OVRLP GO	# IPS genes	IPS Genes in category	IPS GOP	# OF genes	OF Genes in category	OF GOP
Histone H2B	7	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ	9.57E-06	carbohydrate catabolic process	6	TP11, GM2A, ENO2, GAA, PFKM, RPIA	9.92E-04	monosaccharide metabolic process	7	GPD2, UGT1A6A, PGD, HK2, FBP2, DCXR, PMM1	4.17E-02	8	PPP1R3C, MAN2C1, TP11, GANC, ENO2, GAA, PFKM, RPIA	2.20E-03
Histone core	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	1.07E-05	glucose metabolic process	7	PPP1R3C, TP11, GANC, ENO2, GAA, PFKM, RPIA	2.08E-03	hexose metabolic process	6	GPD2, PGD, HK2, FBP2, DCXR, PMM1	7.42E-02	8	PPP1R3C, MAN2C1, TP11, GANC, ENO2, GAA, PFKM, RPIA	1.09E-03
nucleosome core	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	1.82E-05	cellular carbohydrate catabolic process	5	TP11, ENO2, GAA, PFKM, RPIA	2.44E-03							
nucleosome assembly	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	4.06E-04	lysosome	7	CTSZ, GM2A, PSAP, ARSA, GAA, MT1, CTSB	2.73E-03							
chromatin assembly	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	4.70E-04	sphingolipid metabolic process	5	SMPDL3B, GM2A, PSAP, SGPP1, CERK	2.75E-03							
nucleosome organization	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	5.04E-04	lysic vacuole	7	CTSZ, GM2A, PSAP, ARSA, GAA, MT1, CTSB	2.81E-03							
protein-DNA complex assembly	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	5.04E-04	membrane lipid metabolic process	5	SMPDL3B, GM2A, PSAP, SGPP1, CERK	3.09E-03							
DNA packaging	11	HIST1H2BP, HIST1H2BM, HIST1H2BN, HIST1H4K, HIST1H4A, HIST1H2BK, HIST1H2BF, HIST1H2BH, HIST1H2BJ, HIST1H4J, HIST2HAA1	2.23E-03	organophosphate metabolic process	7	ISYNA1, TP11, SMPDL3B, SGPP1, CHKB, TAZ, PGQ	6.40E-03							
stem cell maintenance	4	POU5F1, NODAL, SOX2, KLF4	2.92E-03	glucose catabolic process	4	TP11, ENO2, PFKM, RPIA	1.29E-02							
negative regulation of macromolecule metabolic process	16	MSH5, NODAL, SOX2, TLE4, TGFCP2L1, SAP30, IRAK3, CDKN1A, SALL4, CD59B, POU5F1, HOXA7, BCL3, IgFBP3, DNMT3B, KLF4	3.01E-03	hexose catabolic process	4	TP11, ENO2, PFKM, RPIA	1.29E-02							
stem cell development	4	POU5F1, NODAL, SOX2, KLF4	3.33E-03	monosaccharide catabolic process	4	TP11, ENO2, PFKM, RPIA	1.43E-02							
Sugar/inositol transporter	3	SLC2A6, SLC2A3, SLC2A1	7.46E-03	phospholipid metabolic process	6	ISYNA1, SMPDL3B, SGPP1, CHKB, TAZ, PGQ	1.90E-02							
monosaccharide biosynthetic process	4	GPD2, PGD, FBP2, PMM1	7.83E-03	positive regulation of inflammatory response	3	CD47, C3, LBP	2.12E-02							
embryonic morphogenesis	12	ACVR2B, SALL4, LAMA5, POU5F1, NODAL, TDGF1, TCFAP2A, SOX2, HOXA7, GBX2, SPIN1, EPH42	8.37E-03	alcohol catabolic process	4	TP11, ENO2, PFKM, RPIA	2.33E-02							
coenzyme metabolic process	7	GSR, CBR2, FOLR1, PGD, GSTT3, GLCM, DCXR	1.19E-02	generation of precursor metabolites and energy	7	SLC25A12, PPP1R3C, TP11, ENO2, GAA, PFKM, ETFA	3.70E-02							
alcohol biosynthetic process	4	GPD2, PGD, FBP2, PMM1	1.28E-02	response to wounding	8	HDAC5, LAMB2, C3, MAP9K1, CTSB, LBP, PROS1, CD14	4.58E-02							
negative regulation of RNA metabolic process	10	SAP30, SALL4, POU5F1, NODAL, SOX2, HOXA7, TLE4, DNMT3B, KLF4, TCFCP2L1	2.26E-02	Glycolysis / Gluconeogenesis	4	TP11, ENO2, ALDH2, PFKM	4.79E-02							

embryonic development ending in birth or egg hatching	12	SALL4, POU5F1, NODAL, TGIF1, TCFAP2A, HOXA7, PLCD3, GDX2, GJA1, SPINT1, CDH1, EPHB2	2.61E-02	sphingoid metabolic process	3	GM2A, SGPP1, CERK	4.97E-02
regulation of cell growth	5	CDKN2A, MAPT, SFN, IGFBP3, AHSG	3.38E-02				
blastocyst formation	3	POU5F1, NODAL, CDH1	3.39E-02				
negative regulation of cell differentiation	7	CCND1, POU5F1, NODAL, SOX2, HOXA7, KLF4, TOB1	3.44E-02				
cofactor metabolic process	7	GSR, CBR2, FOLR1, PGD, GSTT3, GCLM, DCXR	3.44E-02				
sugar transmembrane transporter activity	3	SLC2A6, SLC2A3, SLC2A1	3.62E-02				
glutathione metabolic process	3	GSR, GSTT3, GCLM	3.98E-02				
nicotinamide metabolic process	3	CBR2, PGD, DCXR	3.98E-02				
alkaloid metabolic process	3	CBR2, PGD, DCXR	3.98E-02				
nicotinamide nucleotide metabolic process	3	CBR2, PGD, DCXR	3.98E-02				
negative regulation of nitrogen compound metabolic process	11	SAP30, MSH6, SALL4, POU5F1, NODAL, SOX2, HOXA7, TLE4, DNMT3B, KLF4, TCFCP2L1	4.10E-02				
embryonic organ development	8	NODAL, TCFAP2A, SOX2, HOXA7, PLCD3, GDX2, SPINT1, EPHB2	4.17E-02				
hexose biosynthetic process	3	GPD2, FBP2, PMM1	4.29E-02				